#14/a

SEQUENCE LISTING

(1) GEN ERAL INFORMATION:

(i) APPLICANT: Friedman, Jeffrey M.
Lee, Gwo-Hua
Proenca, Ricardo

(ii) TITLE OF INVENTION: DB, THE RECEPTOR FOR LEPTIN, NUCLEIC ACIDS ENCODING THE RECEPTOR, AND USES THEREOF

(iii) NUMBER OF SEQUENCES: 56

(iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: David A. Jackson, Esq.
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(C) CITY: Hackensack
(D) STATE: New Jersey
(E) COUNTRY: USA
(F) ZIP: 07601

(v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: US 08/586,594
(B) FILING DATE:
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Jackson Esq., David A.
(B) REGISTRATION NUMBER: 26,742
(C) REFERENCE/DOCKET NUMBER: 600-1-162

(ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: 201-487-5800
(B) TELEFAX: 201-343-1684

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2529 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:
(B) CLONE: A15 (OB-Ra)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GGGCTCAGGT CGGCGTCGTA CCAGCCGCTG AAGCGGTTCT CCAGGTTCCA GGCGCTCTCG 60

CCATGCCGGA TCAGCACCAG CTTGTAGCTC GTGCCGAATT CGGCACGAGG TTGCTTTGGG 120

AATGAGCAAG GTCAAAACTG CTCTGCACTC ACAGACAACA CTGAAGGGAA GACACTGGCT 180

TCAGTAGTGA AGGCTTCAGT TTTTCGCCAG CTAGGTGTAA ACTGGGACAT AGAGTGCTGG 240

ATGAAAGGGG ACTTGACATT ATTCATCTGT CATATGGAGC CATTACCTAA GAACCCCTTC 300

AAGAATTATG ACTCTAAGGT CCATCTTTTA TATGATCTGC CTGAAGTCAT AGATGATTCG 360

CCTCTGCCCC CACTGAAAGA CAGCTTTCAG ACTGTCCAAT GCAACTGCAG TCTTCGGGGA 420

TGTGAATGTC ATGTGCCGGT ACCCAGAGCC AAACTCAACT ACGCTCTTCT GATGTATTTG 480

GAAATCACAT CTGCCGGTGT GAGTTTTCAG TCACCTCTGA TGTCACTGCA GCCCATGCTT 540

GTTGTGAAAC CCGATCCACC CTTAGGTTTG CATATGGAAG TCACAGATGA TGGTAATTTA 600

AAGATTTCTT GGGACAGCCA AACAATGGCA CCATTTCCGC TTCAATATCA GGTGAAATAT 660

TTAGAGAATT CTACAATTGT AAGAGAGGCT GCTGAAATTG TCTCAGCTAC ATCTCTGCTG 720

GTAGACAGTG TGCTTCCTGG ATCTTCATAT GAGGTCCAGG TGAGGAGCAA GAGACTGGAT 780

GGTTCAGGAG TCTGGAGTGA CTGGAGTTCA CCTCAAGTCT TTACCACACA AGATGTTGTG 840

TATTTTCCAC CCAAAATTCT GACTAGTGTT GGATCGAATG CTTCTTTTCA TTGCATCTAC 900

AAAAACGAAA ACCAGATTAT CTCCTCAAAA CAGATAGTTT GGTGGAGGAA TCTAGCTGAG 960

AAAATCCCTG AGATACAGTA CAGCATTGTG AGTGACCGAG TTAGCAAAGT TACCTTCTCC 1020

AACCTGAAAG CCACCAGACC TCGAGGGAAG TTTACCTATG ACGCAGTGTA CTGCTGCAAT 1080

GAGCAGGCGT GCCATCACCG CTATGCTGAA TTATACGTGA TCGATGTCAA TATCAATATA 1140

TCATGTGAAA CTGACGGGTA CTTAACTAAA ATGACTTGCA GATGGTCACC CAGCACAATC 1200

CAATCACTAG TGGGAAGCAC TGTGCAGCTG AGGTATCACA GGCGCAGCCT GTATTGTCCT 1260

GATAGTCCAT CTATTCATCC TACGTCTGAG CCCAAAAACT GCGTCTTACA GAGAGACGGC 1320

TTTTATGAAT GTGTTTTCCA GCCAATCTTT CTATTATCTG GCTATACAAT GTGGATCAGG 1380

ATCAACCATT CTTTAGGTTC ACTTGACTCG CCACCAACGT GTGTCCTTCC TGACTCCGTA 1440

GTAAAACCAC TACCTCCATC TAACGTAAAA GCAGAGATTA CTGTAAACAC TGGATTATTG 1500

AAAGTATCTT GGGAAAAGCC AGTCTTTCCG GAGAATAACC TTCAATTCCA GATTCGATAT 1560

GGCTTAAGTG GAAAAGAAAT ACAATGGAAG ACACATGAGG TATTCGATGC AAAGTCAAAG 1620

TCTGCCAGCC TGCTGGTGTC AGACCTCTGT GCAGTCTATG TGGTCCAGGT TCGCTGCCGG 1680

CGGTTGGATG GACTAGGATA TTGGAGTAAT TGGAGCAGTC CAGCCTATAC GCTTGTCATG 1740

GATGTAAAAG TTCCTATGAG AGGGCCTGAA TTTTGGAGAA AAATGGATGG GGACGTTACT 1800

AAAAAGGAGA GAAATGTCAC CTTGCTTTGG AAGCCCCTGA CGAAAAATGA CTCACTGTGT 1860

AGTGTGAGGA GGTACGTGGT GAAGCATCGT ACTGCCCACA ATGGGACGTG GTCAGAAGAT 1920

GTGGGAAATC GGACCAATCT CACTTTCCTG TGGACAGAAC CAGCGCACAC TGTTACAGTT 1980

CTGGCTGTCA ATTCCCTCGG CGCTTCCCTT GTGAATTTTA ACCTTACCTT CTCATGGCCC 2040

ATGAGTAAAG TGAGTGCTGT GGAGTCACTC AGTGCTTATC CCCTGAGCAG CAGCTGTGTC 2100

ATCCTTTCCT GGACACTGTC ACCTGATGAT TATAGTCTGT TATATCTGGT TATTGAATGG 2160

AAGATCCTTA ATGAAGATGA TGGAATGAAG TGGCTTAGAA TTCCCTCGAA TGTTAAAAAG 2220

TTTTATATCC ACGATAATTT TATTCCCATC GAGAAATATC AGTTTAGTCT TTACCCAGTA 2280

TTTATGGAAG GAGTTGGAAA ACCAAAGATA ATTAATGGTT TCACCAAAGA TGCTATCGAC 2340

AAGCAGCAGA ATGACGCAGG GCTGTATGTC ATTGTACCCA TAATTATTTC CTCTTGTGTC 2400

CTACTGCTCG GAACACTGTT AATTTCACAC CAGAGAATGA AAAAGTTGTT TTGGGACGAT 2460

GTTCCAAACC CCAAGAATTG TTCCTGGGCA CAAGGACTGA ATTTCCAAAA GAGAACGGAC 2520

ACTCTTTGA 2529

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 842 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:
(B) CLONE: OB-Ra

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Gly Leu Arg Ser Ala Ser Tyr Gln Pro Leu Lys Arg Phe Ser Arg Phe

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1               5                   10                  15

Gln Ala Leu Ser Pro Cys Arg Ile Ser Thr Ser Leu Xaa Leu Val Pro
            20                  25                  30

Asn Ser Ala Arg Gly Cys Phe Gly Asn Glu Gln Gly Gln Asn Cys Ser
        35                  40                  45

Ala Leu Thr Asp Asn Thr Glu Gly Lys Thr Leu Ala Ser Val Val Lys
    50                  55                  60

Ala Ser Val Phe Arg Gln Leu Gly Val Asn Trp Asp Ile Glu Cys Trp
65                  70                  75                  80

Met Lys Gly Asp Leu Thr Leu Phe Ile Cys His Met Glu Pro Leu Pro
                85                  90                  95

Lys Asn Pro Phe Lys Asn Tyr Asp Ser Lys Val His Leu Leu Tyr Asp
            100                 105                 110

Leu Pro Glu Val Ile Asp Asp Ser Pro Leu Pro Pro Leu Lys Asp Ser
        115                 120                 125

Phe Gln Thr Val Gln Cys Asn Cys Ser Leu Arg Gly Cys Glu Cys His
    130                 135                 140

Val Pro Val Pro Arg Ala Lys Leu Asn Tyr Ala Leu Leu Met Tyr Leu
145                 150                 155                 160

Glu Ile Thr Ser Ala Gly Val Ser Phe Gln Ser Pro Leu Met Ser Leu
                165                 170                 175

Gln Pro Met Leu Val Val Lys Pro Asp Pro Pro Leu Gly Leu His Met
            180                 185                 190

Glu Val Thr Asp Asp Gly Asn Leu Lys Ile Ser Trp Asp Ser Gln Thr
        195                 200                 205

Met Ala Pro Phe Pro Leu Gln Tyr Gln Val Lys Tyr Leu Glu Asn Ser
    210                 215                 220

Thr Ile Val Arg Glu Ala Ala Glu Ile Val Ser Ala Thr Ser Leu Leu
225                 230                 235                 240

Val Asp Ser Val Leu Pro Gly Ser Ser Tyr Glu Val Gln Val Arg Ser
                245                 250                 255

Lys Arg Leu Asp Gly Ser Gly Val Trp Ser Asp Trp Ser Ser Pro Gln
            260                 265                 270

Val Phe Thr Thr Gln Asp Val Val Tyr Phe Pro Pro Lys Ile Leu Thr
        275                 280                 285

Ser Val Gly Ser Asn Ala Ser Phe His Cys Ile Tyr Lys Asn Glu Asn
    290                 295                 300

Gln Ile Ile Ser Ser Lys Gln Ile Val Trp Trp Arg Asn Leu Ala Glu
305                 310                 315                 320
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Lys Ile Pro Glu Ile Gln Tyr Ser Ile Val Ser Asp Arg Val Ser Lys
325 330 335

Val Thr Phe Ser Asn Leu Lys Ala Thr Arg Pro Arg Gly Lys Phe Thr
340 345 350

Tyr Asp Ala Val Tyr Cys Cys Asn Glu Gln Ala Cys His His Arg Tyr
355 360 365

Ala Glu Leu Tyr Val Ile Asp Val Asn Ile Asn Ile Ser Cys Glu Thr
370 375 380

Asp Gly Tyr Leu Thr Lys Met Thr Cys Arg Trp Ser Pro Ser Thr Ile
385 390 395 400

Gln Ser Leu Val Gly Ser Thr Val Gln Leu Arg Tyr His Arg Arg Ser
405 410 415

Leu Tyr Cys Pro Asp Ser Pro Ser Ile His Pro Thr Ser Glu Pro Lys
420 425 430

Asn Cys Val Leu Gln Arg Asp Gly Phe Tyr Glu Cys Val Phe Gln Pro
435 440 445

Ile Phe Leu Leu Ser Gly Tyr Thr Met Trp Ile Arg Ile Asn His Ser
450 455 460

Leu Gly Ser Leu Asp Ser Pro Pro Thr Cys Val Leu Pro Asp Ser Val
465 470 475 480

Val Lys Pro Leu Pro Pro Ser Asn Val Lys Ala Glu Ile Thr Val Asn
485 490 495

Thr Gly Leu Leu Lys Val Ser Trp Glu Lys Pro Val Phe Pro Glu Asn
500 505 510

Asn Leu Gln Phe Gln Ile Arg Tyr Gly Leu Ser Gly Lys Glu Ile Gln
515 520 525

Trp Lys Thr His Glu Val Phe Asp Ala Lys Ser Lys Ser Ala Ser Leu
530 535 540

Leu Val Ser Asp Leu Cys Ala Val Tyr Val Val Gln Val Arg Cys Arg
545 550 555 560

Arg Leu Asp Gly Leu Gly Tyr Trp Ser Asn Trp Ser Ser Pro Ala Tyr
565 570 575

Thr Leu Val Met Asp Val Lys Val Pro Met Arg Gly Pro Glu Phe Trp
580 585 590

Arg Lys Met Asp Gly Asp Val Thr Lys Lys Glu Arg Asn Val Thr Leu
595 600 605

Leu Trp Lys Pro Leu Thr Lys Asn Asp Ser Leu Cys Ser Val Arg Arg
610 615 620

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Tyr Val Val Lys His Arg Thr Ala His Asn Gly Thr Trp Ser Glu Asp
625                 630                 635                 640

Val Gly Asn Arg Thr Asn Leu Thr Phe Leu Trp Thr Glu Pro Ala His
                645                 650                 655

Thr Val Thr Val Leu Ala Val Asn Ser Leu Gly Ala Ser Leu Val Asn
            660                 665                 670

Phe Asn Leu Thr Phe Ser Trp Pro Met Ser Lys Val Ser Ala Val Glu
        675                 680                 685

Ser Leu Ser Ala Tyr Pro Leu Ser Ser Ser Cys Val Ile Leu Ser Trp
    690                 695                 700

Thr Leu Ser Pro Asp Asp Tyr Ser Leu Leu Tyr Leu Val Ile Glu Trp
705                 710                 715                 720

Lys Ile Leu Asn Glu Asp Asp Gly Met Lys Trp Leu Arg Ile Pro Ser
                725                 730                 735

Asn Val Lys Lys Phe Tyr Ile His Asp Asn Phe Ile Pro Ile Glu Lys
            740                 745                 750

Tyr Gln Phe Ser Leu Tyr Pro Val Phe Met Glu Gly Val Gly Lys Pro
        755                 760                 765

Lys Ile Ile Asn Gly Phe Thr Lys Asp Ala Ile Asp Lys Gln Gln Asn
    770                 775                 780

Asp Ala Gly Leu Tyr Val Ile Val Pro Ile Ile Ile Ser Ser Cys Val
785                 790                 795                 800

Leu Leu Leu Gly Thr Leu Leu Ile Ser His Gln Arg Met Lys Lys Leu
                805                 810                 815

Phe Trp Asp Asp Val Pro Asn Pro Lys Asn Cys Ser Trp Ala Gln Gly
            820                 825                 830

Leu Asn Phe Gln Lys Arg Thr Asp Thr Leu
        835                 840
```

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2848 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: A40 (OB-Rb)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CTCATTGAGA GTGCCAACGG GAAGGCTTAA TTAACCTTTG GAANTGAGTC CGAAGAGTCT 60

GGAAGTNTGT AAGATGGAAG ATACTATACA AGATACTTCA GAGCTGTACA TTCTTCCAGG 120

GATGTAGGCT AGCAGTTATT TCATTAGTAT ATGTCTATTT TAGAATGGGA AGAATTAGGA 180

AGATGAATGG AGCCTGTGTC TTTCACTACT CTCCCAGGAG GTTCCAGAAT AGCNAAAGTG 240

TCAGCCAGAA TTCTTGAAGT CATAGACTGG AGTTAGAGAT GAACATAAGC TCATGTTAAG 300

CCTGGGTTAC TTCTTATCAT CCTTAATTTT GAAAGCTAAG AGGGCCTAAC CATCAAGAAC 360

GTCCTGGAGG AAAGAATGTT TTTAACGCCA TTATTCAGTC AAAGAAATTA AGACTTGAGA 420

GAAATGCTCA TTTCTTCTCT CATGATGGCT CCTTACACCT TACTTCTACC GTACGATCCA 480

TGNGGCCCTA CCCACGCAGG ATACATGCAT CTATATGAGA GTGTCTNCCC CTTCTAACTC 540

AGAGACTCTT GTTCTAGTCT GTGNTATAAA ATTCAGCTTG TGGAAGCTTT CTGAGGGGTT 600

GGCAGCATTC AATTTTACCT GCAATAGGTA AAGGTAATCT TTTGGGAAGT GAAGAGTGTT 660

ATTAGACATT TCAGAAAGAA CAAACAGGAT TGGGGCTGCT ATGTGTTCTA CACAGGAATC 720

TTCCATAACA CAGAATAATT TATGTAGATA GAGACAAGAT GGAAATGCCC AGGGCCCCAA 780

AATAGCCGCT GTTATTTGTT AACCTTCAAG GTTTTCTGTT TGTTTATCTG TTTCTTGCGC 840

AGGATCATCT TCCAAGCACA TCCTGGGGGA ACAGTGGCAG AGTCACTCGA GTTCATGAAA 900

CTATGGTGAC ATCTGAGCTT CCTTGGTTCT TCACAGAACA TAAGCAGTTC CTTTGCTTGC 960

TTGTTAGATG AGAAAACTTC CTTGTCAGTC TGTCTCTACG ACTAGAATGG AAAGCCTTAC 1020

TACTTCCTAT GTATTCTTAA TATTTCAAAT GTCCTAATTA TGTTTGGCTT CTCTGTCTTT 1080

AAGGGATTTA GTCTCTGGAT TTGAAGAAAT AAATAAATAA ATAAAGGAAA ACTAATTTTC 1140

TCGTGCCGGA TGACTGCTAG CTGAGCTCAG GCCTACTGCA TTCTACATTT CGACTCTCTC 1200

CCTCTTCCCC AGTGCTTTAG CACTGGACTG GGCAGTNCCT GGCCTGGTCT AACTCCTGTT 1260

TCCTGGTGGG AATGTATAAT AAGAACTCCA TGAGTTCTGG TATAAACACT GTGGTCTGTG 1320

TGCTAATTAA ATCTNGTGTT TCCTACAGCC CCTGACGAAA AATGACTCAC TGTGTAGTGT 1380

GAGGAGGTAC GTGGTGAAGC ATCGTACTGC CCACAATGGG ACGTGGTCAG AAGATGTGGG 1440

AAATCGGACC AATCTCACTT TCCTGTGGAC AGAACCAGCG CACACTGTTA CAGTTCTGGC 1500

TGTCAATTCC CTCGGCGCTT CCCTTGTGAA TTTTAACCTT ACCTTCTCAT GGCCCATGAG 1560

TAAAGTGAGT GCTGTGGAGT CACTCAGTGC TTATCCCCTG AGCAGCAGCT GTGTCATCCT 1620

TTCCTGGACA CTGTCACCTG ATGATTATAG TCTGTTATAT CTGGTTATTG AATGGAAGAT 1680

CCTTAATGAA GATGATGGAA TGAAGTGGCT TAGAATTCCC TCGAATGTTA AAAAGTTTTA 1740

TATCCACGAT AATTTTATTC CCATCGAGAA ATATCAGTTT AGTCTTTACC CAGTATTTAT 1800

GGAAGGAGTT GGAAAACCAA AGATAATTAA TGGTTTCACC AAAGATGCTA TCGACAAGCA 1860

GCAGAATGAC GCAGGGCTGT ATGTCATTGT ACCCATAATT ATTTCCTCTT GTGTCCTACT 1920

GCTCGGAACA CTGTTAATTT CACACCAGAG AATGAAAAAG TTGTTTTGGG ACGATGTTCC 1980

AAACCCCAAG AATTGTTCCT GGGCACAAGG ACTGAATTTC CAAAAGCCTG AAACATTNGA 2040

GCATCTTTTT ACCAAGCATG CAGAATCAGT GATATTTGGT CCTCTTCTTC TGGAGCCTGA 2100

ACCCATTTCA GAAGAAATCA GTGTCGATAC AGCTTGGAAA AATAAAGATG AGATGGTCCC 2160

AGCAGCTATG GTCTCCCTNC TNNGGACCAC ACCAGACCCT GAAAGCAGTT CTATTTGTNT 2220

TAGTGACCAG TGTAACAGTG CTAACTTCTC TGGGTCTCAG AGCACCCAGG TAACCTGTGA 2280

GGATGAGTGT CAGAGACAAC CCTCAGTTAA ATATGCAACT CTGGTCAGCA ACGATAAACT 2340

AGTGGAAACT GATGAAGAGC AAGGGTTTAT CCATAGTCCT GTCAGCAACT GCATCTCCAG 2400

TAATCATTCC CCACTGAGGC AGTCTTTCTC TAGCAGCTCC TGGGAGACAG AGGCCCAGAC 2460

ATTTTTCCTT TTATCAGACC AGCAACCCAC CATGATTTCA CCACAACTTT CATTCTCGGG 2520

GTTGGATGAG CTTTTGGAAC TGGAGGGAAG TTTTCCTGAA GAAAATCACA GGGAGNAGTC 2580

TGTCTGTTAT CTAGGAGTCA CCTCCGTCCN CAGAAGAGAG AGTGGTGTGC TTTTGACTGG 2640

TGAGGCAGGA ATCCTGTGCA CATTCCCAGC CCAGTGTCTG TTCAGTGACA TCAGGATCCT 2700

CCAGGAGAGA TGCTCACACT TTGTAGAAAA TAATTTGAGT TTAGGGACCT CTGGTGAGAA 2760

CTTTGGTCCT AACATGCCCC AATTCCAAAC CTGTTCCACG CACAGTCACA AGATAATGGA 2820

GAATAAGATG TGTGACTTAA CTGTGTAA 2848

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 581 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:
(B) CLONE: OB-Rb

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Leu Arg Asp Leu Val Ser Gly Phe Glu Glu Ile Asn Lys Ile Lys Glu
1 5 10 15

Asn Phe Ser Arg Ala Gly Leu Leu Ala Glu Leu Arg Pro Thr Ala Phe
20 25 30

Tyr Ile Ser Thr Leu Ser Leu Phe Pro Ser Ala Leu Ala Leu Asp Trp
35 40 45

Ala Val Pro Gly Leu Val Leu Leu Phe Pro Gly Gly Asn Val Glu Leu
50 55 60

His Glu Phe Trp Tyr Lys His Cys Gly Leu Cys Ala Asn Ile Xaa Cys
65 70 75 80

Phe Leu Gln Pro Leu Thr Lys Asn Asp Ser Leu Cys Ser Val Arg Arg
85 90 95

Tyr Val Val Lys His Arg Thr Ala His Asn Gly Thr Trp Ser Glu Asp
100 105 110

Val Gly Asn Arg Thr Asn Leu Thr Phe Leu Trp Thr Glu Pro Ala His
115 120 125

Thr Val Thr Val Leu Ala Val Asn Ser Leu Gly Ala Ser Leu Val Asn
130 135 140

Phe Asn Leu Thr Phe Ser Trp Pro Met Ser Lys Val Ser Ala Val Glu
145 150 155 160

Ser Leu Ser Ala Tyr Pro Leu Ser Ser Ser Cys Val Ile Leu Ser Trp
165 170 175

Thr Leu Ser Pro Asp Asp Tyr Ser Leu Leu Tyr Leu Val Ile Glu Trp
180 185 190

Lys Ile Leu Asn Glu Asp Asp Gly Met Lys Trp Leu Arg Ile Pro Ser
195 200 205

Asn Val Lys Lys Phe Tyr Ile His Asp Asn Phe Ile Pro Ile Glu Lys
210 215 220

Tyr Gln Phe Ser Leu Tyr Pro Val Phe Met Glu Gly Val Gly Lys Pro
225 230 235 240

Lys Ile Ile Asn Gly Phe Thr Lys Asp Ala Ile Asp Lys Gln Gln Asn
245 250 255

Asp Ala Gly Leu Tyr Val Ile Val Pro Ile Ile Ile Ser Ser Cys Val
260 265 270

```
Leu Leu Leu Gly Thr Leu Leu Ile Ser His Gln Arg Met Lys Lys Leu
        275                 280                 285

Phe Trp Asp Asp Val Pro Asn Pro Lys Asn Cys Ser Trp Ala Gln Gly
    290                 295                 300

Leu Asn Phe Gln Lys Pro Glu Thr Phe Glu Gln Leu Phe Thr Lys His
305                 310                 315                 320

Ala Glu Ser Val Ile Phe Gly Pro Leu Leu Leu Glu Pro Glu Pro Ile
                325                 330                 335

Ser Glu Glu Ile Ser Val Asp Thr Ala Trp Lys Asn Lys Asp Glu Met
            340                 345                 350

Val Pro Ala Ala Met Val Ser Leu Leu Trp Thr Thr Pro Asp Pro Glu
        355                 360                 365

Ser Ser Ser Ile Cys Ile Ser Asp Gln Cys Asn Ser Ala Asn Phe Ser
    370                 375                 380

Gly Ser Gln Ser Thr Gln Val Cys Glu Asp Glu Cys Gln Arg Gln Pro
385                 390                 395                 400

Ser Val Lys Tyr Ala Thr Leu Val Ser Asn Asp Lys Leu Val Glu Thr
                405                 410                 415

Asp Glu Glu Gln Gly Phe Ile His Ser Pro Val Ser Asn Cys Ile Ser
            420                 425                 430

Ser Asn His Ser Pro Leu Arg Gln Ser Phe Ser Ser Ser Ser Trp Glu
        435                 440                 445

Thr Glu Ala Gln Thr Phe Phe Leu Leu Ser Asp Gln Gln Pro Thr Met
    450                 455                 460

Ile Ser Pro Gln Leu Ser Phe Ser Gly Leu Asp Glu Leu Leu Glu Leu
465                 470                 475                 480

Glu Gly Ser Phe Pro Glu Glu Asn His Arg Glu Lys Ser Val Cys Tyr
                485                 490                 495

Leu Gly Val Thr Ser Val Asn Arg Arg Glu Ser Gly Val Leu Leu Thr
            500                 505                 510

Gly Glu Ala Gly Ile Leu Cys Thr Phe Pro Ala Gln Cys Leu Phe Ser
        515                 520                 525

Asp Ile Arg Ile Leu Gln Glu Arg Cys Ser His Phe Val Glu Asn Asn
    530                 535                 540

Leu Ser Leu Gly Thr Ser Gly Glu Asn Phe Gly Pro Tyr Met Pro Gln
545                 550                 555                 560

Phe Gln Thr Cys Ser Thr His Ser His Lys Ile Met Glu Asn Lys Met
                565                 570                 575
```

Cys Asp Phe Thr Val
580

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 961 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:
(B) CLONE: A6 (OB-Rc)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

TTTAAGGGAT TTAGTCTCTG GATTTGAAGA AATAAATAAA TAAATAAAGG AAAACTAATT 60

TTCTCGTGCC GGATGACTGC TAGCTGAGCT CAGGCCTACT GCATTCTACA TTTCGACTCT 120

CTCCCTCTTC CCCAGTGCTT TAGCACTGGA CTGGGCAGTN CCTGGCCTGG TCTAACTCCT 180

GTTTCCTGGT GGGAATGTAT AATAAGAACT CCATGAGTTC TGGTATAAAC ACTGTGGTCT 240

GTGTGCTAAT TAAATCTNGT GTTTCCTACA GCCCCTGACG AAAAATGACT CACTGTGTAG 300

TGTGAGGAGG TACGTGGTGA AGCATCGTAC TGCCCACAAT GGGACGTGGT CAGAAGATGT 360

GGGAAATCGG ACCAATCTCA CTTTCCTGTG GACAGAACCA GCGCACACTG TTACAGTTCT 420

GGCTGTCAAT TCCCTCGGCG CTTCCCTTGT GAATTTTAAC CTTACCTTCT CATGGCCCAT 480

GAGTAAAGTG AGTGCTGTGG AGTCACTCAG TGCTTATCCC CTGAGCAGCA GCTGTGTCAT 540

CCTTTCCTGG ACACTGTCAC CTGATGATTA TAGTCTGTTA TATCTGGTTA TTGAATGGAA 600

GATCCTTAAT GAAGATGATG GAATGAAGTG GCTTAGAATT CCCTCGAATG TTAAAAAGTT 660

TTATATCCAC GATAATTTTA TTCCCATCGA GAAATATCAG TTTAGTCTTT ACCCAGTATT 720

TATGGAAGGA GTTGGAAAAC CAAAGATAAT TAATGGTTTC ACCAAAGATG CTATCGACAA 780

GCAGCAGAAT GACGCAGGGC TGTATGTCAT TGTACCCATA ATTATTTCCT CTTGTGTCCT 840

ACTGCTCGGA ACACTGTTAA TTTCACACCA GAGAATGAAA AAGTTGTTTT GGGACGATGT 900

TCCAAACCCC AAGAATTGTT CCTGGGCACA AGGACTGAAT TTCCAAAAGG TCACTGTTTA 960

A 961

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 319 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:
(B) CLONE: OB-Rc

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

```
Leu Arg Asp Leu Val Ser Gly Phe Glu Glu Ile Asn Lys Xaa Ile Lys
1               5                  10                  15

Glu Asn Xaa Phe Ser Arg Ala Gly Xaa Leu Leu Ala Glu Leu Arg Pro
            20                  25                  30

Thr Ala Phe Tyr Ile Ser Thr Leu Ser Leu Phe Pro Ser Ala Leu Ala
        35                  40                  45

Leu Asp Trp Ala Val Pro Gly Leu Val Xaa Leu Leu Phe Pro Gly Gly
    50                  55                  60

Asn Val Xaa Xaa Glu Leu His Glu Phe Trp Tyr Lys His Cys Gly Leu
65                  70                  75                  80

Cys Ala Asn Xaa Ile Xaa Cys Phe Leu Gln Pro Leu Thr Lys Asn Asp
                85                  90                  95

Ser Leu Cys Ser Val Arg Arg Tyr Val Val Lys His Arg Thr Ala His
            100                 105                 110

Asn Gly Thr Trp Ser Glu Asp Val Gly Asn Arg Thr Asn Leu Thr Phe
        115                 120                 125

Leu Trp Thr Glu Pro Ala His Thr Val Thr Val Leu Ala Val Asn Ser
    130                 135                 140

Leu Gly Ala Ser Leu Val Asn Phe Asn Leu Thr Phe Ser Trp Pro Met
145                 150                 155                 160

Ser Lys Val Ser Ala Val Glu Ser Leu Ser Ala Tyr Pro Leu Ser Ser
                165                 170                 175

Ser Cys Val Ile Leu Ser Trp Thr Leu Ser Pro Asp Asp Tyr Ser Leu
            180                 185                 190
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Leu Tyr Leu Val Ile Glu Trp Lys Ile Leu Asn Glu Asp Asp Gly Met
195 200 205

Lys Trp Leu Arg Ile Pro Ser Asn Val Lys Lys Phe Tyr Ile His Asp
210 215 220

Asn Phe Ile Pro Ile Glu Lys Tyr Gln Phe Ser Leu Tyr Pro Val Phe
225 230 235 240

Met Glu Gly Val Gly Lys Pro Lys Ile Ile Asn Gly Phe Thr Lys Asp
245 250 255

Ala Ile Asp Lys Gln Gln Asn Asp Ala Gly Leu Tyr Val Ile Val Pro
260 265 270

Ile Ile Ile Ser Ser Cys Val Leu Leu Leu Gly Thr Leu Leu Ile Ser
275 280 285

His Gln Arg Met Lys Lys Leu Phe Trp Asp Asp Val Pro Asn Pro Lys
290 295 300

Asn Cys Ser Trp Ala Gln Gly Leu Asn Phe Gln Lys Val Thr Val
305 310 315

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2703 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:
(B) CLONE: A8 (OB-Rd)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

ATGATGTGTC AGAAATTCTA TGTGGTTTTG TTACACTGGG AATTTCTTTA TGTGATAGCT 60

GCACTTAACC TGGCATATCC AATCTCTCCC TGGAAATTTA AGTTGTTTTG TGGACCACCG 120

AACACAACCG ATGACTCCTT TCTCTCACCT GCTGGAGCCC CAAACAATGC CTCGGCTTTG 180

AAGGGGGCTT CTGAAGCAAT TGTTGAAGCT AAATTTAATT CAAGTGGTAT CTACGTTCCT 240

GAGTTATCCA AAACAGTCTT CCACTGTTGC TTTGGGAATG AGCAAGGTCA AAACTGCTCT 300

GCACTCACAG ACAACACTGA AGGGAAGACA CTGGCTTCAG TAGTGAAGGC TTCAGTTTTT 360

CGCCAGCTAG GTGTAAACTG GGACATAGAG TGCTGGATGA AAGGGGACTT GACATTATTC 420

ATCTGTCATA TGGAGCCATT ACCTAAGAAC CCCTTCAAGA ATTATGACTC TAAGGTCCAT 480

CTTTTATATG ATCTGCCTGA AGTCATAGAT GATTCGCCTC TGCCCCCACT GAAAGACAGC 540

TTTCAGACTG TCCAATGCAA CTGCAGTCTT CGGGGATGTG AATGTCATGT GCCGGTACCC 600

AGAGCCAAAC TCAACTACGC TCTTCTGATG TATTTGGAAA TCACATCTGC CGGTGTGAGT 660

TTTCAGTCAC CTCTGATGTC ACTGCAGCCC ATGCTTGTTG TGAAACCCGA TCCACCCTTA 720

GGTTTGCATA TGGAAGTCAC AGATGATGGT AATTTAAAGA TTTCTTGGGA CAGCCAAACA 780

ATGGCACCAT TTCCGCTTCA ATATCAGGTG AAATATTTAG AGAATTCTAC AATTGTAAGA 840

GAGGCTGCTG AAATTGTCTC AGCTACATCT CTGCTGGTAG ACAGTGTGCT TCCTGGATCT 900

TCATATGAGG TCCAGGTGAG GAGCAAGAGA CTGGATGGTT CAGGAGTCTG GAGTGACTGG 960

AGTTCACCTC AAGTCTTTAC CACACAAGAT GTTGTGTATT TTCCACCCAA AATTCTGACT 1020

AGTGTTGGAT CGAATGCTTC TTTTCATTGC ATCTACAAAA ACGAAAACCA GATTATCTCC 1080

TCAAAACAGA TAGTTTGGTG GAGGAATCTA GCTGAGAAAA TCCCTGAGAT ACAGTACAGC 1140

ATTGTGAGTG ACCGAGTTAG CAAAGTTACC TTCTCCAACC TGAAAGCCAC CAGACCTCGA 1200

GGGAAGTTTA CCTATGACGC AGTGTACTGC TGCAATGAGC AGGCGTGCCA TCACCGCTAT 1260

GCTGAATTAT ACGTGATCGA TGTCAATATC AATATATCAT GTGAAACTGA CGGGTACTTA 1320

ACTAAAATGA CTTGCAGATG GTCACCCAGC ACAATCCAAT CACTAGTGGG AAGCACTGTG 1380

CAGCTGAGGT ATCACAGGCG CAGCCTGTAT TGTCCTGATA GTCCATCTAT TCATCCTACG 1440

TCTGAGCCCA AAAACTGCGT CTTACAGAGA GACGGCTTTT ATGAATGTGT TTTCCAGCCA 1500

ATCTTTCTAT TATCTGGCTA TACAATGTGG ATCAGGATCA ACCATTCTTT AGGTTCACTT 1560

GACTCGCCAC CAACGTGTGT CCTTCCTGAC TCCGTAGTAA AACCACTACC TCCATCTAAC 1620

GTAAAAGCAG AGATTACTGT AAACACTGGA TTATTGAAAG TATCTTGGGA AAAGCCAGTC 1680

TTTCCGGAGA ATAACCTTCA ATTCCAGATT CGATATGGCT TAAGTGGAAA AGAAATACAA 1740

TGGAAGACAC ATGAGGTATT CGATGCAAAG TCAAAGTCTG CCAGCCTGCT GGTGTCAGAC 1800

CTCTGTGCAG TCTATGTGGT CCAGGTTCGC TGCCGGCGGT TGGATGGACT AGGATATTGG 1860

AGTAATTGGA GCAGTCCAGC CTATACGCTT GTCATGGATG TAAAAGTTCC TATGAGAGGG 1920

CCTGAATTTT GGAGAAAAAT GGATGGGGAC GTTACTAAAA AGGAGAGAAA TGTCACCTTG 1980

CTTTGGAAGC CCCTGACGAA AAATGACTCA CTGTGTAGTG TGAGGAGGTA CGTGGTGAAG 2040

CATCGTACTG CCCACAATGG GACGTGGTCA GAAGATGTGG GAAATCGGAC CAATCTCACT 2100

TTCCTGTGGA CAGAACCAGC GCACACTGTT ACAGTTCTGG CTGTCAATTC CCTCGGCGCT 2160

TCCCTTGTGA ATTTTAACCT TACCTTCTCA TGGCCCATGA GTAAAGTGAG TGCTGTGGAG 2220

TCACTCAGTG CTTATCCCCT GAGCAGCAGC TGTGTCATCC TTTCCTGGAC ACTGTCACCT 2280

GATGATTATA GTCTGTTATA TCTGGTTATT GAATGGAAGA TCCTTAATGA AGATGATGGA 2340

ATGAAGTGGC TTAGAATTCC CTCGAATGTT AAAAAGTTTT ATATCCACGA TAATTTTATT 2400

CCCATCGAGA AATATCAGTT TAGTCTTTAC CCAGTATTTA TGGAAGGAGT TGGAAAACCA 2460

AAGATAATTA ATGGTTTCAC CAAAGATGCT ATCGACAAGC AGCAGAATGA CGCAGGGCTG 2520

TATGTCATTG TACCCATAAT TATTTCCTCT TGTGTCCTAC TGCTCGGAAC ACTGTTAATT 2580

TCACACCAGA GAATGAAAAA GTTGTTTTGG GACGATGTTC CAAACCCCAA GAATTGTTCC 2640

TGGGCACAAG GACTGAATTT CCAAAAGGAT ATATCTTTAC ATGAAGTTTT TATTTTCAGA 2700

TAG 2703

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 900 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:
(B) CLONE: OB-Rd

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Met Cys Gln Lys Phe Tyr Val Val Leu Leu His Trp Glu Phe Leu
1 5 10 15

Tyr Val Ile Ala Ala Leu Asn Leu Ala Tyr Pro Ile Ser Pro Trp Lys
20 25 30

Phe Lys Leu Phe Cys Gly Pro Pro Asn Thr Thr Asp Asp Ser Phe Leu
35 40 45

Ser Pro Ala Gly Ala Pro Asn Asn Ala Ser Ala Leu Lys Gly Ala Ser
50 55 60

Glu Ala Ile Val Glu Ala Lys Phe Asn Ser Ser Gly Ile Tyr Val Pro

65 70 75 80

Glu Leu Ser Lys Thr Val Phe His Cys Cys Phe Gly Asn Glu Gln Gly
85 90 95

Gln Asn Cys Ser Ala Leu Thr Asp Asn Thr Glu Gly Lys Thr Leu Ala
100 105 110

Ser Val Val Lys Ala Ser Val Phe Arg Gln Leu Gly Val Asn Trp Asp
115 120 125

Ile Glu Cys Trp Met Lys Gly Asp Leu Thr Leu Phe Ile Cys His Met
130 135 140

Glu Pro Leu Pro Lys Asn Pro Phe Lys Asn Tyr Asp Ser Lys Val His
145 150 155 160

Leu Leu Tyr Asp Leu Pro Glu Val Ile Asp Asp Ser Pro Leu Pro Pro
165 170 175

Leu Lys Asp Ser Phe Gln Thr Val Gln Cys Asn Cys Ser Leu Arg Gly
180 185 190

Cys Glu Cys His Val Pro Val Pro Arg Ala Lys Leu Asn Tyr Ala Leu
195 200 205

Leu Met Tyr Leu Glu Ile Thr Ser Ala Gly Val Ser Phe Gln Ser Pro
210 215 220

Leu Met Ser Leu Gln Pro Met Leu Val Val Lys Pro Asp Pro Pro Leu
225 230 235 240

Gly Leu His Met Glu Val Thr Asp Asp Gly Asn Leu Lys Ile Ser Trp
245 250 255

Asp Ser Gln Thr Met Ala Pro Phe Pro Leu Gln Tyr Gln Val Lys Tyr
260 265 270

Leu Glu Asn Ser Thr Ile Val Arg Glu Ala Ala Glu Ile Val Ser Ala
275 280 285

Thr Ser Leu Leu Val Asp Ser Val Leu Pro Gly Ser Ser Tyr Glu Val
290 295 300

Gln Val Arg Ser Lys Arg Leu Asp Gly Ser Gly Val Trp Ser Asp Trp
305 310 315 320

Ser Ser Pro Gln Val Phe Thr Thr Gln Asp Val Val Tyr Phe Pro Pro
325 330 335

Lys Ile Leu Thr Ser Val Gly Ser Asn Ala Ser Phe His Cys Ile Tyr
340 345 350

Lys Asn Glu Asn Gln Ile Ile Ser Ser Lys Gln Ile Val Trp Trp Arg
355 360 365

Asn Leu Ala Glu Lys Ile Pro Glu Ile Gln Tyr Ser Ile Val Ser Asp
370 375 380

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Arg Val Ser Lys Val Thr Phe Ser Asn Leu Lys Ala Thr Arg Pro Arg
385                 390                 395                 400

Gly Lys Phe Thr Tyr Asp Ala Val Tyr Cys Cys Asn Glu Gln Ala Cys
                405                 410                 415

His His Arg Tyr Ala Glu Leu Tyr Val Ile Asp Val Asn Ile Asn Ile
            420                 425                 430

Ser Cys Glu Thr Asp Gly Tyr Leu Thr Lys Met Thr Cys Arg Trp Ser
        435                 440                 445

Pro Ser Thr Ile Gln Ser Leu Val Gly Ser Thr Val Gln Leu Arg Tyr
    450                 455                 460

His Arg Arg Ser Leu Tyr Cys Pro Asp Ser Pro Ser Ile His Pro Thr
465                 470                 475                 480

Ser Glu Pro Lys Asn Cys Val Leu Gln Arg Asp Gly Phe Tyr Glu Cys
                485                 490                 495

Val Phe Gln Pro Ile Phe Leu Leu Ser Gly Tyr Thr Met Trp Ile Arg
            500                 505                 510

Ile Asn His Ser Leu Gly Ser Leu Asp Ser Pro Pro Thr Cys Val Leu
        515                 520                 525

Pro Asp Ser Val Val Lys Pro Leu Pro Pro Ser Asn Val Lys Ala Glu
    530                 535                 540

Ile Thr Val Asn Thr Gly Leu Leu Lys Val Ser Trp Glu Lys Pro Val
545                 550                 555                 560

Phe Pro Glu Asn Asn Leu Gln Phe Gln Ile Arg Tyr Gly Leu Ser Gly
                565                 570                 575

Lys Glu Ile Gln Trp Lys Thr His Glu Val Phe Asp Ala Lys Ser Lys
            580                 585                 590

Ser Ala Ser Leu Leu Val Ser Asp Leu Cys Ala Val Tyr Val Val Gln
        595                 600                 605

Val Arg Cys Arg Arg Leu Asp Gly Leu Gly Tyr Trp Ser Asn Trp Ser
    610                 615                 620

Ser Pro Ala Tyr Thr Leu Val Met Asp Val Lys Val Pro Met Arg Gly
625                 630                 635                 640

Pro Glu Phe Trp Arg Lys Met Asp Gly Asp Val Thr Lys Lys Glu Arg
                645                 650                 655

Asn Val Thr Leu Leu Trp Lys Pro Leu Thr Lys Asn Asp Ser Leu Cys
            660                 665                 670

Ser Val Arg Arg Tyr Val Val Lys His Arg Thr Ala His Asn Gly Thr
        675                 680                 685
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Trp Ser Glu Asp Val Gly Asn Arg Thr Asn Leu Thr Phe Leu Trp Thr
    690                 695                 700

Glu Pro Ala His Thr Val Thr Val Leu Ala Val Asn Ser Leu Gly Ala
705                 710                 715                 720

Ser Leu Val Asn Phe Asn Leu Thr Phe Ser Trp Pro Met Ser Lys Val
                725                 730                 735

Ser Ala Val Glu Ser Leu Ser Ala Tyr Pro Leu Ser Ser Ser Cys Val
            740                 745                 750

Ile Leu Ser Trp Thr Leu Ser Pro Asp Asp Tyr Ser Leu Leu Tyr Leu
        755                 760                 765

Val Ile Glu Trp Lys Ile Leu Asn Glu Asp Asp Gly Met Lys Trp Leu
    770                 775                 780

Arg Ile Pro Ser Asn Val Lys Lys Phe Tyr Ile His Asp Asn Phe Ile
785                 790                 795                 800

Pro Ile Glu Lys Tyr Gln Phe Ser Leu Tyr Pro Val Phe Met Glu Gly
                805                 810                 815

Val Gly Lys Pro Lys Ile Ile Asn Gly Phe Thr Lys Asp Ala Ile Asp
            820                 825                 830

Lys Gln Gln Asn Asp Ala Gly Leu Tyr Val Ile Val Pro Ile Ile Ile
        835                 840                 845

Ser Ser Cys Val Leu Leu Leu Gly Thr Leu Leu Ile Ser His Gln Arg
    850                 855                 860

Met Lys Lys Leu Phe Trp Asp Asp Val Pro Asn Pro Lys Asn Cys Ser
865                 870                 875                 880

Trp Ala Gln Gly Leu Asn Phe Gln Lys Asp Ile Ser Leu His Glu Val
                885                 890                 895

Phe Ile Phe Arg
            900
```

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2461 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: A20 (OB-Re)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GAGGAATCGT TCTGCAAATC CAGGTGTACA CCTCTGAAGA AAGATGATGT GTCAGAAATT 60

CTATGTGGTT TTGTTACACT GGGAATTTCT TTATGTGATA GCTGCACTTA ACCTGGCATA 120

TCCAATCTCT CCCTGGAAAT TTAAGTTGTT TTGTGGACCA CCGAACACAA CCGATGACTC 180

CTTTCTCTCA CCTGCTGGAG CCCCAAACAA TGCCTCGGCT TTGAAGGGGG CTTCTGAAGC 240

AATTGTTGAA GCTAAATTTA ATTCAAGTGG TATCTACGTT CCTGAGTTAT CCAAAACAGT 300

CTTCCACTGT TGCTTTGGGA ATGAGCAAGG TCAAAACTGC TCTGCACTCA CAGACAACAC 360

TGAAGGGAAG ACACTGGCTT CAGTAGTGAA GGCTTCAGTT TTTCGCCAGC TAGGTGTAAA 420

CTGGGACATA GAGTGCTGGA TGAAAGGGGA CTTGACATTA TTCATCTGTC ATATGGAGCC 480

ATTACCTAAG AACCCCTTCA AGAATTATGA CTCTAAGGTC CATCTTTTAT ATGATCTGCC 540

TGAAGTCATA GATGATTCGC CTCTGCCCCC ACTGAAAGAC AGCTTTCAGA CTGTCCAATG 600

CAACTGCAGT CTTCGGGGAT GTGAATGTCA TGTGCCGGTA CCCAGAGCCA AACTCAACTA 660

CGCTCTTCTG ATGTATTTGG AAATCACATC TGCCGGTGTG AGTTTTCAGT CACCTCTGAT 720

GTCACTGCAG CCCATGCTTG TTGTGAAACC CGATCCACCC TTAGGTTTGC ATATGGAAGT 780

CACAGATGAT GGTAATTTAA AGATTTCTTG GGACAGCCAA ACAATGGCAC CATTTCCGCT 840

TCAATATCAG GTGAAATATT TAGAGAATTC TACAATTGTA AGAGAGGCTG CTGAAATTGT 900

CTCAGCTACA TCTCTGCTGG TAGACAGTGT GCTTCCTGGA TCTTCATATG AGGTCCAGGT 960

GAGGAGCAAG AGACTGGATG GTTCAGGAGT CTGGAGTGAC TGGAGTTCAC CTCAAGTCTT 1020

TACCACACAA GATGTTGTGT ATTTTCCACC CAAAATTCTG ACTAGTGTTG GATCGAATGC 1080

TTCTTTTCAT TGCATCTACA AAAACGAAAA CCAGATTATC TCCTCAAAAC AGATAGTTTG 1140

GTGGAGGAAT CTAGCTGAGA AAATCCCTGA GATACAGTAC AGCATTGTGA GTGACCGAGT 1200

TAGCAAAGTT ACCTTCTCCA ACCTGAAAGC CACCAGACCT CGAGGGAAGT TTACCTATGA 1260

CGCAGTGTAC TGCTGCAATG AGCAGGCGTG CCATCACCGC TATGCTGAAT TATACGTGAT 1320

CGATGTCAAT ATCAATATAT CATGTGAAAC TGACGGGTAC TTAACTAAAA TGACTTGCAG 1380

ATGGTCACCC AGCACAATCC AATCACTAGT GGGAAGCACT GTGCAGCTGA GGTATCACAG 1440

GCGCAGCCTG TATTGTCCTG ATAGTCCATC TATTCATCCT ACGTCTGAGC CCAAAAACTG 1500

CGTCTTACAG AGAGACGGCT TTTATGAATG TGTTTTCCAG CCAATCTTTC TATTATCTGG 1560

CTATACAATG TGGATCAGGA TCAACCATTC TTTAGGTTCA CTTGACTCGC CACCAACGTG 1620

TGTCCTTCCT GACTCCGTAG TAAAACCACT ACCTCCATCT AACGTAAAAG CAGAGATTAC 1680

TGTAAACACT GGATTATTGA AAGTATCTTG GGAAAAGCCA GTCTTTCCGG AGAATAACCT 1740

TCAATTCCAG ATTCGATATG GCTTAAGTGG AAAAGAAATA CAATGGAAGA CACATGAGGT 1800

ATTCGATGCA AAGTCAAAGT CTGCCAGCCT GCTGGTGTCA GACCTCTGTG CAGTCTATGT 1860

GGTCCAGGTT CGCTGCCGGC GGTTGGATGG ACTAGGATAT TGGAGTAATT GGAGCAGTCC 1920

AGCCTATACG CTTGTCATGG ATGTAAAAGT TCCTATGAGA GGGCCTGAAT TTTGGAGAAA 1980

AATGGATGGG GACGTTACTA AAAAGGAGAG AAATGTCACC TTGCTTTGGA AGCCCCTGAC 2040

GAAAAATGAC TCACTGTGTA GTGTGAGGAG GTACGTGGTG AAGCATCGTA CTGCCCACAA 2100

TGGGACGTGG TCAGAAGATG TGGGAAATCG GACCAATCTC ACTTTCCTGT GGACAGAACC 2160

AGCGCACACT GTTACAGTTC TGGCTGTCAA TTCCCTCGGC GCTTCCCTTG TGAATTTTAA 2220

CCTTACCTTC TCATGGCCCA TGAGTAAAGT GAGTGCTGTG GAGTCACTCA GTGCTTATCC 2280

CCTGAGCAGC AGCTGTGTCA TCCTTTCCTG GACACTGTCA CCTGATGATT ATAGTCTGTT 2340

ATATCTGGTT ATTGAATGGA AGATCCTTAA TGAAGATGAT GGAATGAAGT GGCTTAGAAT 2400

TCCCTCGAAT GTTAAAAAGT TTTATATCCA CGGTATGTGT ACTGTACTTT TCATGGATTA 2460

G 2461

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 805 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:
(B) CLONE: OB-Re

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met Met Cys Gln Lys Phe Tyr Val Val Leu Leu His Trp Glu Phe Leu
1 5 10 15

Tyr Val Ile Ala Ala Leu Asn Leu Ala Tyr Pro Ile Ser Pro Trp Lys

```
            20                  25                  30

Phe Lys Leu Phe Cys Gly Pro Pro Asn Thr Thr Asp Asp Ser Phe Leu
        35                  40                  45

Ser Pro Ala Gly Ala Pro Asn Asn Ala Ser Ala Leu Lys Gly Ala Ser
    50                  55                  60

Glu Ala Ile Val Glu Ala Lys Phe Asn Ser Ser Gly Ile Tyr Val Pro
65                  70                  75                  80

Glu Leu Ser Lys Thr Val Phe His Cys Cys Phe Gly Asn Glu Gln Gly
                85                  90                  95

Gln Asn Cys Ser Ala Leu Thr Asp Asn Thr Glu Gly Lys Thr Leu Ala
            100                 105                 110

Ser Val Val Lys Ala Ser Val Phe Arg Gln Leu Gly Val Asn Trp Asp
        115                 120                 125

Ile Glu Cys Trp Met Lys Gly Asp Leu Thr Leu Phe Ile Cys His Met
    130                 135                 140

Glu Pro Leu Pro Lys Asn Pro Phe Lys Asn Tyr Asp Ser Lys Val His
145                 150                 155                 160

Leu Leu Tyr Asp Leu Pro Glu Val Ile Asp Asp Ser Pro Leu Pro Pro
                165                 170                 175

Leu Lys Asp Ser Phe Gln Thr Val Gln Cys Asn Cys Ser Leu Arg Gly
            180                 185                 190

Cys Glu Cys His Val Pro Val Pro Arg Ala Lys Leu Asn Tyr Ala Leu
        195                 200                 205

Leu Met Tyr Leu Glu Ile Thr Ser Ala Gly Val Ser Phe Gln Ser Pro
    210                 215                 220

Leu Met Ser Leu Gln Pro Met Leu Val Val Lys Pro Asp Pro Pro Leu
225                 230                 235                 240

Gly Leu His Met Glu Val Thr Asp Asp Gly Asn Leu Lys Ile Ser Trp
                245                 250                 255

Asp Ser Gln Thr Met Ala Pro Phe Pro Leu Gln Tyr Gln Val Lys Tyr
            260                 265                 270

Leu Glu Asn Ser Thr Ile Val Arg Glu Ala Ala Glu Ile Val Ser Ala
        275                 280                 285

Thr Ser Leu Leu Val Asp Ser Val Leu Pro Gly Ser Ser Tyr Glu Val
    290                 295                 300

Gln Val Arg Ser Lys Arg Leu Asp Gly Ser Gly Val Trp Ser Asp Trp
305                 310                 315                 320

Ser Ser Pro Gln Val Phe Thr Thr Gln Asp Val Val Tyr Phe Pro Pro
                325                 330                 335
```

Lys Ile Leu Thr Ser Val Gly Ser Asn Ala Ser Phe His Cys Ile Tyr
340 345 350

Lys Asn Glu Asn Gln Ile Ile Ser Ser Lys Gln Ile Val Trp Trp Arg
355 360 365

Asn Leu Ala Glu Lys Ile Pro Glu Ile Gln Tyr Ser Ile Val Ser Asp
370 375 380

Arg Val Ser Lys Val Thr Phe Ser Asn Leu Lys Ala Thr Arg Pro Arg
385 390 395 400

Gly Lys Phe Thr Tyr Asp Ala Val Tyr Cys Cys Asn Glu Gln Ala Cys
405 410 415

His His Arg Tyr Ala Glu Leu Tyr Val Ile Asp Val Asn Ile Asn Ile
420 425 430

Ser Cys Glu Thr Asp Gly Tyr Leu Thr Lys Met Thr Cys Arg Trp Ser
435 440 445

Pro Ser Thr Ile Gln Ser Leu Val Gly Ser Thr Val Gln Leu Arg Tyr
450 455 460

His Arg Arg Ser Leu Tyr Cys Pro Asp Ser Pro Ser Ile His Pro Thr
465 470 475 480

Ser Glu Pro Lys Asn Cys Val Leu Gln Arg Asp Gly Phe Tyr Glu Cys
485 490 495

Val Phe Gln Pro Ile Phe Leu Leu Ser Gly Tyr Thr Met Trp Ile Arg
500 505 510

Ile Asn His Ser Leu Gly Ser Leu Asp Ser Pro Pro Thr Cys Val Leu
515 520 525

Pro Asp Ser Val Val Lys Pro Leu Pro Pro Ser Asn Val Lys Ala Glu
530 535 540

Ile Thr Val Asn Thr Gly Leu Leu Lys Val Ser Trp Glu Lys Pro Val
545 550 555 560

Phe Pro Glu Asn Asn Leu Gln Phe Gln Ile Arg Tyr Gly Leu Ser Gly
565 570 575

Lys Glu Ile Gln Trp Lys Thr His Glu Val Phe Asp Ala Lys Ser Lys
580 585 590

Ser Ala Ser Leu Leu Val Ser Asp Leu Cys Ala Val Tyr Val Val Gln
595 600 605

Val Arg Cys Arg Arg Leu Asp Gly Leu Gly Tyr Trp Ser Asn Trp Ser
610 615 620

Ser Pro Ala Tyr Thr Leu Val Met Asp Val Lys Val Pro Met Arg Gly
625 630 635 640

Pro Glu Phe Trp Arg Lys Met Asp Gly Asp Val Thr Lys Lys Glu Arg
645 650 655

Asn Val Thr Leu Leu Trp Lys Pro Leu Thr Lys Asn Asp Ser Leu Cys
660 665 670

Ser Val Arg Arg Tyr Val Val Lys His Arg Thr Ala His Asn Gly Thr
675 680 685

Trp Ser Glu Asp Val Gly Asn Arg Thr Asn Leu Thr Phe Leu Trp Thr
690 695 700

Glu Pro Ala His Thr Val Thr Val Leu Ala Val Asn Ser Leu Gly Ala
705 710 715 720

Ser Leu Val Asn Phe Asn Leu Thr Phe Ser Trp Pro Met Ser Lys Val
725 730 735

Ser Ala Val Glu Ser Leu Ser Ala Tyr Pro Leu Ser Ser Ser Cys Val
740 745 750

Ile Leu Ser Trp Thr Leu Ser Pro Asp Asp Tyr Ser Leu Leu Tyr Leu
755 760 765

Val Ile Glu Trp Lys Ile Leu Asn Glu Asp Asp Gly Met Lys Trp Leu
770 775 780

Arg Ile Pro Ser Asn Val Lys Lys Phe Tyr Ile His Gly Met Cys Thr
785 790 795 800

Val Leu Phe Met Asp
805

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 8 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: C-terminal

(vii) IMMEDIATE SOURCE:
(B) CLONE: OB-Ra

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Asn Phe Gln Lys Arg Thr Asp Leu

1 5

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 276 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: C-terminal

(vii) IMMEDIATE SOURCE:
(B) CLONE: OB-Rb

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

```
Asn Phe Gln Lys Pro Glu Thr Phe Glu Gln Leu Phe Thr Lys His Ala
1               5                  10                  15

Glu Ser Val Ile Phe Gly Pro Leu Leu Leu Glu Pro Glu Pro Ile Ser
            20                  25                  30

Glu Glu Ile Ser Val Asp Thr Ala Trp Lys Asn Lys Asp Glu Met Val
        35                  40                  45

Pro Ala Ala Met Val Ser Leu Leu Trp Thr Thr Pro Asp Pro Glu Ser
    50                  55                  60

Ser Ser Ile Cys Ile Ser Asp Gln Cys Asn Ser Ala Asn Phe Ser Gly
65                  70                  75                  80

Ser Gln Ser Thr Gln Val Cys Glu Asp Glu Cys Gln Arg Gln Pro Ser
                85                  90                  95

Val Lys Tyr Ala Thr Leu Val Ser Asn Asp Lys Leu Val Glu Thr Asp
            100                 105                 110

Glu Glu Gln Gly Phe Ile His Ser Pro Val Ser Asn Cys Ile Ser Ser
        115                 120                 125

Asn His Ser Pro Leu Arg Gln Ser Phe Ser Ser Ser Ser Trp Glu Thr
    130                 135                 140

Glu Ala Gln Thr Phe Phe Leu Leu Ser Asp Gln Gln Pro Thr Met Ile
145                 150                 155                 160

Ser Pro Gln Leu Ser Phe Ser Gly Leu Asp Glu Leu Leu Glu Leu Glu
                165                 170                 175
```

Gly Ser Phe Pro Glu Glu Asn His Arg Glu Lys Ser Val Cys Tyr Leu
180 185 190

Gly Val Thr Ser Val Asn Arg Arg Glu Ser Gly Val Leu Leu Thr Gly
195 200 205

Glu Ala Gly Ile Leu Cys Thr Phe Pro Ala Gln Cys Leu Phe Ser Asp
210 215 220

Ile Arg Ile Leu Gln Glu Arg Cys Ser His Phe Val Glu Asn Asn Leu
225 230 235 240

Ser Leu Gly Thr Ser Gly Glu Asn Phe Gly Pro Tyr Met Pro Gln Phe
245 250 255

Gln Thr Cys Ser Thr His Ser His Lys Ile Met Glu Asn Lys Met Cys
260 265 270

Asp Phe Thr Val
275

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: C-terminal

(vii) IMMEDIATE SOURCE:
(B) CLONE: OB-Rc

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Asn Phe Gln Lys Val Thr Val
1 5

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: C-terminal

(vii) IMMEDIATE SOURCE:
(B) CLONE: OB-Rd

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Asn Phe Gln Lys Asp Ile Ser His Glu Val Phe Ile Phe Arg
1 5 10

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: C-terminal

(vii) IMMEDIATE SOURCE:
(B) CLONE: OB-Re

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Phe Tyr Ile His Gly Met Cys Thr Val Leu Phe Met Asp
1 5 10

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 8 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(vii) IMMEDIATE SOURCE:
(B) CLONE: OB-Ra/db/db

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Pro Gln Lys Arg Thr Asp Thr Leu
1 5

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(vii) IMMEDIATE SOURCE:
(B) CLONE: OB-Rb/wt

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Pro Gln Lys Pro Glu Thr
1 5

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

GATGGAGGGA AA 12

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GATGGAGGTA AA 12

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

ATCTTGGGTT CTCTGAAGAA 20

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

GAGATTGTCA GTCACAGCCT C 21

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

ATCTGAATTG GAATCAAATA CAC 23

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

AAATCTGTTA TCCTTCTGAA AC 22

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

ACACTGTTAA TTTCACACCA GAG 23

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

AGTCATTCAA ACCATTAGTT TAGG 24

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

TGGATAAACC CTTGCTCTTC A 21

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

TGAACACAAC AACATAAAGC CC 22

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

AGGCTCCCTC AGGGCCAC 18

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

GTGACTGAAT GAAGATGTAA TATAC 25

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

TGTTATATCT GGTTATTGAA TGG 23

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

CATTAAATGA TTTATTATCA GAATTGC 27

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Glu Pro Leu Pro Lys Asn Pro Phe Lys Asn Tyr Asp Ser Lys
1 5 10

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

His Arg Arg Ser Leu Tyr Cys Pro Asp Ser Pro Ser Ile His Pro Thr
1 5 10 15

Ser Glu Pro Lys
20

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Gln Arg Met Lys Lys Leu Phe Trp Asp Asp Val Pro Asn Pro Lys Asn
1 5 10 15

Cys Ser Trp

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 166 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:
(B) CLONE: 7

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

AGGGNAAGCG CCGAGGGAAT TGACAGCCAG AACTGTAACA GTGTGCGCTG GTTCTGTCCA 60

CAGGAAAGTG AGATTGGTCC GATTTCCCAC ATCTTCTGAC CACGTCCCAT TGTGGGCAGT 120

ACGATGCTTC ACCACGTACC TCCTCACACT ACACAGTGAG TCATTT 166

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 320 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:
(B) CLONE: 11

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

GGTGAAGCAT CGTACTGCCC ACAATGGGAC GTGGTCAGAA GATGTGGGAA ATCGGACCAA 60

TCTCACTTTC CTGTGGACAG AACCAGCGCA CACTGTTACA GTTCTGGCTG TCAATTCCCT 120

CGGCGCTTCC CTTGTGAATT TTAACCTTAC CTTCTCATGG CCCATGAGTA AAGTGAGTGC 180

TGTGGAGTCA CTCAGTGCTT ATCCCCTGAG CAGCAGCTGT GTCATCCTTT CCTGGACACT 240

GTCACCTGAT GATTATAGTC TGTTATATCT GGTTATTGAA TGGAAGATCC TTAATGAAGA 300

TGATGGAATG AAGTGGCTTA 320

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 158 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:
(B) CLONE: 42

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

GATTACTGGA GATGCAGTTG CTGACAGGAC TATGGATAAA CCCTTGCTCT TCATCAGTTT 60

CCACTAGTTT ATCGTTGCTG ACCAGAGTTG CATATTTAAC TGAGGGTTGT CTCTGACACT 120

CATCCTCACA GGTTACCTGG GTGCTCTGAG ACCCAGAG 158

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 192 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:
(B) CLONE: 46

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

AGAGAGATCC CTGACCCTAG TTAGATCTGT TTTCAGGCTC TGTGTTCATT TGATGTTCAG 60

AAGTCAGCAA GGTTCTCATA TGTCCTGAGT TAGTAAGATG TCTCAGGGTT CCCCCATCAG 120

CTAACAACCA CTTTGACATG AGAAGGCAGA AAGTTAAAGA ACACTACTTG GTGTTTTACT 180

TAAAGATACG AG 192

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 168 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:
(B) CLONE: 58

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

AGACTGACAA GGAAGTTTTC TCATCTAACA AGCAAGCAAA GGAACTGCTT ATGTNCTGTG 60

ANGAACCAAG GNAGCTCAGA TGTCACCATA GTCATCATGA ACTCGAGTGA CTCTGCCACT 120

GTTCCCCCAG GATGTGCTTG GANGATAATC CTGCGCAAGA AACAGATA 168

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 259 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:
(B) CLONE: S3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

AGAATTATGA CTCTAAGGTC CATCTTTTAT ATGATCTGCC TGAAGTCATA GATGATTCGC 60

CTCTGCCCCC ACTGAAAGAC AGNTTTCAGA CTGTCCAATG NAACTGCAGT CTTCGGGGAT 120

GTGAATGTCA TGTGCCAGTA CCCAGAGCCA AACTCAACTA CGCTCTTCTG ATGTATTTGG 180

NAATCACATC TGCCGGTGTG AGTTTTCAGT CACCTCTGAT GTCACTGCAG CCCATGCTTG 240

TTGTGAAACC CGATCCACC 259

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 250 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:
(B) CLONE: S14

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

CTTCAACAAT TGGTTCAGAA GCCCCCTTCA AAGCCGAGGC ATTGTTTGGG GCTCCAGCAG 60

GTGAGAGAAA GGAGTCATCG GTTGTGTTCG GTGGTCCACA AAACAACTTA AATTTCCAGG 120

GAGAGATTGG ATATGCCAGG TTAAGTGCAG CTATCACATA AAGAAATTCC CAGTGTAACA 180

AAACCACATA GANTTTCTAA CACATCATCT TTCTTCAGAG GTGTACACCT GGATTTGCAG 240

AACGATTCCT 250

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

CCGAGGGAAT TGACAGCC 18

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

CTCACTGTGT AGTGTGAGGA GG 22

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

TCCTGTGGAC AGAACCAGC 19

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

TGACACAGCT GCTGCTCAG 19

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

GGTCTCAGAG CACCCAGGTA 20

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

AGAGAGATCC CTGACCCTAG TT 22

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

AACTTTCTGC CTTCCTTCTC ATGTCA 26

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

TTTCTCATCT AACAAGCAAG CA 22

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

ATCTGTTTCT TGCGCAGGAT 20

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

CATTGTTTGG GGCTCCAG 18

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

AATCGTTCTG CAAATCCAGG 20

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

TGAAGTCATA GATGATTCGC C 21

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

GTTCGTACCC GACGTCACTG 20

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 894 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:
(B) CLONE: OB-R

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

```
Met Met Cys Gln Lys Phe Tyr Val Val Leu Leu His Trp Glu Phe Leu
1               5                  10                  15

Tyr Val Ile Ala Ala Leu Asn Leu Ala Tyr Pro Ile Ser Pro Trp Lys
            20                  25                  30
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Phe Lys Leu Phe Cys Gly Pro Pro Asn Thr Thr Asp Asp Ser Phe Leu
        35                  40                  45

Ser Pro Ala Gly Ala Pro Asn Asn Ala Ser Ala Leu Lys Gly Ala Ser
    50                  55                  60

Glu Ala Ile Val Glu Ala Lys Phe Asn Ser Ser Gly Ile Tyr Val Pro
65                  70                  75                  80

Glu Leu Ser Lys Thr Val Phe His Cys Cys Phe Gly Asn Glu Gln Gly
                85                  90                  95

Gln Asn Cys Ser Ala Leu Thr Asp Asn Thr Glu Gly Lys Thr Leu Ala
            100                 105                 110

Ser Val Val Lys Ala Ser Val Phe Arg Gln Leu Gly Val Asn Trp Asp
        115                 120                 125

Ile Glu Cys Trp Met Lys Gly Asp Leu Thr Leu Phe Ile Cys His Met
    130                 135                 140

Glu Pro Leu Pro Lys Asn Pro Phe Lys Asn Tyr Asp Ser Lys Val His
145                 150                 155                 160

Leu Leu Tyr Asp Leu Pro Glu Val Ile Asp Asp Ser Pro Leu Pro Pro
                165                 170                 175

Leu Lys Asp Ser Phe Gln Thr Val Gln Cys Asn Cys Ser Leu Arg Gly
            180                 185                 190

Cys Glu Cys His Val Pro Val Pro Arg Ala Lys Leu Asn Tyr Ala Leu
        195                 200                 205

Leu Met Tyr Leu Glu Ile Thr Ser Ala Gly Val Ser Phe Gln Ser Pro
    210                 215                 220

Leu Met Ser Leu Gln Pro Met Leu Val Val Lys Pro Asp Pro Pro Leu
225                 230                 235                 240

Gly Leu His Met Glu Val Thr Asp Asp Gly Asn Leu Lys Ile Ser Trp
                245                 250                 255

Asp Ser Gln Thr Met Ala Pro Phe Pro Leu Gln Tyr Gln Val Lys Tyr
            260                 265                 270

Leu Glu Asn Ser Thr Ile Val Arg Glu Ala Ala Glu Ile Val Ser Ala
        275                 280                 285

Thr Ser Leu Leu Val Asp Ser Val Leu Pro Gly Ser Ser Tyr Glu Val
    290                 295                 300

Gln Val Arg Ser Lys Arg Leu Asp Gly Ser Gly Val Trp Ser Asp Trp
305                 310                 315                 320

Ser Ser Pro Gln Val Phe Thr Thr Gln Asp Val Val Tyr Phe Pro Pro
                325                 330                 335

Lys Ile Leu Thr Ser Val Gly Ser Asn Ala Ser Phe His Cys Ile Tyr
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            340                 345                 350

Lys Asn Glu Asn Gln Ile Ile Ser Ser Lys Gln Ile Val Trp Trp Arg
        355                 360                 365

Asn Leu Ala Glu Lys Ile Pro Glu Ile Gln Tyr Ser Ile Val Ser Asp
    370                 375                 380

Arg Val Ser Lys Val Thr Phe Ser Asn Leu Lys Ala Thr Arg Pro Arg
385                 390                 395                 400

Gly Lys Phe Thr Tyr Asp Ala Val Tyr Cys Cys Asn Glu Gln Ala Cys
                405                 410                 415

His His Arg Tyr Ala Glu Leu Tyr Val Ile Asp Val Asn Ile Asn Ile
            420                 425                 430

Ser Cys Glu Thr Asp Gly Tyr Leu Thr Lys Met Thr Cys Arg Trp Ser
        435                 440                 445

Pro Ser Thr Ile Gln Ser Leu Val Gly Ser Thr Val Gln Leu Arg Tyr
    450                 455                 460

His Arg Arg Ser Leu Tyr Cys Pro Asp Ser Pro Ser Ile His Pro Thr
465                 470                 475                 480

Ser Glu Pro Lys Asn Cys Val Leu Gln Arg Asp Gly Phe Tyr Glu Cys
                485                 490                 495

Val Phe Gln Pro Ile Phe Leu Leu Ser Gly Tyr Thr Met Trp Ile Arg
            500                 505                 510

Ile Asn His Ser Leu Gly Ser Leu Asp Ser Pro Pro Thr Cys Val Leu
        515                 520                 525

Pro Asp Ser Val Val Lys Pro Leu Pro Pro Ser Asn Val Lys Ala Glu
    530                 535                 540

Ile Thr Val Asn Thr Gly Leu Leu Lys Val Ser Trp Glu Lys Pro Val
545                 550                 555                 560

Phe Pro Glu Asn Asn Leu Gln Phe Gln Ile Arg Tyr Gly Leu Ser Gly
                565                 570                 575

Lys Glu Ile Gln Trp Lys Thr His Glu Val Phe Asp Ala Lys Ser Lys
            580                 585                 590

Ser Ala Ser Leu Leu Val Ser Asp Leu Cys Ala Val Tyr Val Val Gln
        595                 600                 605

Val Arg Cys Arg Arg Leu Asp Gly Leu Gly Tyr Trp Ser Asn Trp Ser
    610                 615                 620

Ser Pro Ala Tyr Thr Leu Val Met Asp Val Lys Val Pro Met Arg Gly
625                 630                 635                 640

Pro Glu Phe Trp Arg Lys Met Asp Gly Asp Val Thr Lys Lys Glu Arg
                645                 650                 655
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Asn Val Thr Leu Leu Trp Lys Pro Leu Thr Lys Asn Asp Ser Leu Cys
            660                 665                 670

Ser Val Arg Arg Tyr Val Val Lys His Arg Thr Ala His Asn Gly Thr
        675                 680                 685

Trp Ser Glu Asp Val Gly Asn Arg Thr Asn Leu Thr Phe Leu Trp Thr
    690                 695                 700

Glu Pro Ala His Thr Val Thr Val Leu Ala Val Asn Ser Leu Gly Ala
705                 710                 715                 720

Ser Leu Val Asn Phe Asn Leu Thr Phe Ser Trp Pro Met Ser Lys Val
                725                 730                 735

Ser Ala Val Glu Ser Leu Ser Ala Tyr Pro Leu Ser Ser Ser Cys Val
            740                 745                 750

Ile Leu Ser Trp Thr Leu Ser Pro Asp Asp Tyr Ser Leu Leu Tyr Leu
        755                 760                 765

Val Ile Glu Trp Lys Ile Leu Asn Glu Asp Asp Gly Met Lys Trp Leu
    770                 775                 780

Arg Ile Pro Ser Asn Val Lys Lys Phe Tyr Ile His Asp Asn Phe Ile
785                 790                 795                 800

Pro Ile Glu Lys Tyr Gln Phe Ser Leu Tyr Pro Val Phe Met Glu Gly
                805                 810                 815

Val Gly Lys Pro Lys Ile Ile Asn Gly Phe Thr Lys Asp Ala Ile Asp
            820                 825                 830

Lys Gln Gln Asn Asp Ala Gly Leu Tyr Val Ile Val Pro Ile Ile Ile
        835                 840                 845

Ser Ser Cys Val Leu Leu Leu Gly Thr Leu Leu Ile Ser His Gln Arg
    850                 855                 860

Met Lys Lys Leu Phe Trp Asp Asp Val Pro Asn Pro Lys Asn Cys Ser
865                 870                 875                 880

Trp Ala Gln Gly Leu Asn Phe Gln Lys Arg Thr Asp Thr Leu
                885                 890
```

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1165 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

```
Met Ile Cys Gln Lys Phe Cys Val Val Leu Leu His Trp Glu Phe Ile
1               5                  10                  15

Tyr Val Ile Thr Ala Phe Asn Leu Ser Tyr Pro Ile Thr Pro Trp Arg
            20                  25                  30

Phe Lys Leu Ser Cys Met Pro Pro Asn Ser Thr Tyr Asp Tyr Phe Leu
        35                  40                  45

Leu Pro Ala Gly Leu Ser Lys Asn Thr Ser Asn Ser Asn Gly His Tyr
    50                  55                  60

Glu Thr Ala Val Glu Pro Lys Phe Asn Ser Ser Gly Thr His Phe Ser
65                  70                  75                  80

Asn Leu Ser Lys Thr Thr Phe His Cys Cys Phe Arg Ser Glu Gln Asp
                85                  90                  95

Arg Asn Cys Ser Leu Cys Ala Asp Asn Ile Glu Gly Lys Thr Phe Val
            100                 105                 110

Ser Thr Val Asn Ser Leu Val Phe Gln Gln Ile Asp Ala Asn Trp Asn
        115                 120                 125

Ile Gln Cys Trp Leu Lys Gly Asp Leu Lys Leu Phe Ile Cys Tyr Val
    130                 135                 140

Glu Ser Leu Phe Lys Asn Leu Phe Arg Asn Tyr Asn Tyr Lys Val His
145                 150                 155                 160

Leu Leu Tyr Val Leu Pro Glu Val Leu Glu Asp Ser Pro Leu Val Pro
                165                 170                 175

Gln Lys Gly Ser Phe Gln Met Val His Cys Asn Cys Ser Val His Glu
            180                 185                 190

Cys Cys Glu Cys Leu Val Pro Val Pro Thr Ala Lys Leu Asn Asp Thr
        195                 200                 205

Leu Leu Met Cys Leu Lys Ile Thr Ser Gly Gly Val Ile Phe Gln Ser
    210                 215                 220

Pro Leu Met Ser Val Gln Pro Ile Asn Met Val Lys Pro Asp Pro Pro
225                 230                 235                 240

Leu Gly Leu His Met Glu Ile Thr Asp Asp Gly Asn Leu Lys Ile Ser
                245                 250                 255

Trp Ser Ser Pro Pro Leu Val Pro Phe Pro Leu Gln Tyr Gln Val Lys
            260                 265                 270

Tyr Ser Glu Asn Ser Thr Thr Val Ile Arg Glu Ala Asp Lys Ile Val
        275                 280                 285

Ser Ala Thr Ser Leu Leu Val Asp Ser Ile Leu Pro Gly Ser Ser Tyr
    290                 295                 300
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Glu Val Gln Val Arg Gly Lys Arg Leu Asp Gly Pro Gly Ile Trp Ser
305 310 315 320

Asp Trp Ser Thr Pro Arg Val Phe Thr Thr Gln Asp Val Ile Tyr Phe
325 330 335

Pro Pro Lys Ile Leu Thr Ser Val Gly Ser Asn Val Ser Phe His Cys
340 345 350

Ile Tyr Lys Lys Glu Asn Lys Ile Val Pro Ser Lys Glu Ile Val Trp
355 360 365

Trp Met Asn Leu Ala Glu Lys Ile Pro Gln Ser Gln Tyr Asp Val Val
370 375 380

Ser Asp His Val Ser Lys Val Thr Phe Phe Asn Leu Asn Glu Thr Lys
385 390 395 400

Pro Arg Gly Lys Phe Thr Tyr Asp Ala Val Tyr Cys Cys Asn Glu His
405 410 415

Glu Cys His His Arg Tyr Ala Glu Leu Tyr Val Ile Asp Val Asn Ile
420 425 430

Asn Ile Ser Cys Glu Thr Asp Gly Tyr Leu Thr Lys Met Thr Cys Arg
435 440 445

Trp Ser Thr Ser Thr Ile Gln Ser Leu Ala Glu Ser Thr Leu Gln Leu
450 455 460

Arg Tyr His Arg Ser Ser Leu Tyr Cys Ser Asp Ile Pro Ser Ile His
465 470 475 480

Pro Ile Ser Glu Pro Lys Asp Cys Tyr Leu Gln Ser Asp Gly Phe Tyr
485 490 495

Glu Cys Ile Phe Gln Pro Ile Phe Leu Leu Ser Gly Tyr Thr Met Trp
500 505 510

Ile Arg Ile Asn His Ser Leu Gly Ser Leu Asp Ser Pro Pro Thr Cys
515 520 525

Val Leu Pro Asp Ser Val Val Lys Pro Leu Pro Pro Ser Ser Val Lys
530 535 540

Ala Glu Ile Thr Ile Asn Ile Gly Leu Leu Lys Ile Ser Trp Glu Lys
545 550 555 560

Pro Val Phe Pro Glu Asn Asn Leu Gln Phe Gln Ile Arg Tyr Gly Leu
565 570 575

Ser Gly Lys Glu Val Gln Trp Lys Met Tyr Glu Val Tyr Asp Ala Lys
580 585 590

Ser Lys Ser Val Ser Leu Pro Val Pro Asp Leu Cys Ala Val Tyr Ala
595 600 605

Val Gln Val Arg Cys Lys Arg Leu Asp Gly Leu Gly Tyr Trp Ser Asn
610 615 620

Trp Ser Asn Pro Ala Tyr Thr Val Val Met Asp Ile Lys Val Pro Met
625 630 635 640

Arg Gly Pro Glu Phe Trp Arg Ile Ile Asn Gly Asp Thr Met Lys Lys
645 650 655

Glu Lys Asn Val Thr Leu Leu Trp Lys Pro Leu Met Lys Asn Asp Ser
660 665 670

Leu Cys Ser Val Gln Arg Tyr Val Ile Asn His His Thr Ser Cys Asn
675 680 685

Gly Thr Trp Ser Glu Asp Val Gly Asn His Thr Lys Phe Thr Phe Leu
690 695 700

Trp Thr Glu Gln Ala His Thr Val Thr Val Leu Ala Ile Asn Ser Ile
705 710 715 720

Gly Ala Ser Val Ala Asn Phe Asn Leu Thr Phe Ser Trp Pro Met Ser
725 730 735

Lys Val Asn Ile Val Gln Ser Leu Ser Ala Tyr Pro Leu Asn Ser Ser
740 745 750

Cys Val Ile Val Ser Trp Ile Leu Ser Pro Ser Asp Tyr Lys Leu Met
755 760 765

Tyr Phe Ile Ile Glu Trp Lys Asn Leu Asn Glu Asp Gly Glu Ile Lys
770 775 780

Trp Leu Arg Ile Ser Ser Ser Val Lys Lys Tyr Tyr Ile His Asp His
785 790 795 800

Phe Ile Pro Ile Glu Lys Tyr Gln Phe Ser Leu Tyr Pro Ile Phe Met
805 810 815

Glu Gly Val Gly Lys Pro Lys Ile Ile Asn Ser Phe Thr Gln Asp Asp
820 825 830

Ile Glu Lys His Gln Ser Asp Ala Gly Leu Tyr Val Ile Val Pro Val
835 840 845

Ile Ile Ser Ser Ser Ile Leu Leu Leu Gly Thr Leu Leu Ile Ser His
850 855 860

Gln Arg Met Lys Lys Leu Phe Trp Glu Asp Val Pro Asn Pro Lys Asn
865 870 875 880

Cys Ser Trp Ala Gln Gly Leu Asn Phe Gln Lys Pro Glu Thr Phe Glu
885 890 895

His Leu Phe Ile Lys His Thr Ala Ser Val Thr Cys Gly Pro Leu Leu
900 905 910

Leu Glu Pro Glu Thr Ile Ser Glu Asp Ile Ser Val Asp Thr Ser Trp
915 920 925

Lys Asn Lys Asp Glu Met Met Pro Thr Thr Val Val Ser Leu Leu Ser
930 935 940

Thr Thr Asp Leu Glu Lys Gly Ser Val Cys Ile Ser Asp Gln Phe Asn
945 950 955 960

Ser Val Asn Phe Ser Glu Ala Glu Gly Thr Glu Val Thr Tyr Glu Ala
965 970 975

Glu Ser Gln Arg Gln Pro Phe Val Lys Tyr Ala Thr Leu Ile Ser Asn
980 985 990

Ser Lys Pro Ser Glu Thr Gly Glu Glu Gln Gly Leu Ile Asn Ser Ser
995 1000 1005

Val Thr Lys Cys Phe Ser Ser Lys Asn Ser Pro Leu Lys Asp Ser Phe
1010 1015 1020

Ser Asn Ser Ser Trp Glu Ile Glu Ala Gln Ala Phe Phe Ile Leu Ser
1025 1030 1035 1040

Asp Gln His Pro Asn Ile Ile Ser Pro His Leu Thr Phe Ser Glu Gly
1045 1050 1055

Leu Asp Glu Leu Leu Lys Leu Glu Gly Asn Phe Pro Glu Glu Asn Asn
1060 1065 1070

Asp Lys Lys Ser Ile Tyr Tyr Leu Gly Val Thr Ser Ile Lys Lys Arg
1075 1080 1085

Glu Ser Gly Val Leu Leu Thr Asp Lys Ser Arg Val Ser Cys Pro Phe
1090 1095 1100

Pro Ala Pro Cys Leu Phe Thr Asp Ile Arg Val Leu Gln Asp Ser Cys
1105 1110 1115 1120

Ser His Phe Val Glu Asn Asn Ile Asn Leu Gly Thr Ser Ser Lys Lys
1125 1130 1135

Thr Phe Ala Ser Tyr Met Pro Gln Phe Gln Thr Cys Ser Thr Gln Thr
1140 1145 1150

His Lys Ile Met Glu Asn Lys Met Cys Asp Leu Thr Val
1155 1160 1165